Patent claims

1. A homoserine transsuccinylase which, as compared with a homoserine transsuccinylase wild-type enzyme, exhibits a reduced sensitivity toward L-methionine or SAM, with the wild-type enzyme possessing an amino acid sequence which comprises a constituent sequence TyrGlnXaaThrPro, with the Thr of this constituent sequence being between position 285 and 310 of the amino acid sequence and with position 1 being the starting methionine, characterized in that it exhibits a change of at least 2 amino acids as compared with the wild-type enzyme, with this change being in the Thr of the constituent sequence or C-terminally thereof.

2. A homoserine transsuccinylase as claimed in claim 1, characterized in that it exhibits a change of at least 5 amino acids, preferably of at least 10 amino acids.

3. A homoserine transsuccinylase as claimed in claim 1 or 2, characterized in that it exhibits a resistance toward the inhibitors SAM and/or L-methionine which is increased (increased Ki) at least 2-fold as compared with that of the wild-type enzyme.

4. A homoserine transsuccinylase as claimed in one of claims 1 to 3, characterized in that it contains one of the mutations listed in Table 1.

5. A metA allele which encodes a homoserine transsuccinylase as claimed in one of claims 1 to 4.

6. A plasmid, characterized in that it contains a metA allele as claimed in claim 5 together with a promoter.

7. A microorganism strain, characterized in that it contains a feedback-resistant metA allele as claimed in claim 5.

8. A microorganism strain as claimed in claim 7, characterized in that it is a Gram-negative bacterial strain, preferably E. coli.

9. A method for preparing L-methionine or SAM by culturing a microorganism strain as claimed in claim 7 or 8.